

GenCore version 4.5
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v

OM protein - protein search, using sw model.

Run on: September 4, 2002, 16:13:06 ; Search time 101.54 Seconds

(without alignments)
48.262 Million cell updates/sec

Title: US-09-052-089A-6

Perfect score: 293
Sequence: 1 LSQCTICSDFFDHSDVAI.....IOWFETAPSRTCPQCRLQVG 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71;*

1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID

Description

RESULT	1
T0807	TRAF interacting protein - Fugu rubripes
C;Species: Fugu rubripes	
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 02-Sep-2000	
C;Accession: T30807	
R;Cottage, A.J.; Clark, M.; Hawker, K.; Umrania, Y.; Wheeler, D.; Bishop, M.; Elgar, FEBS Lett. 443, 370-374, 1999	
A;Title: Three receptor genes for plasminogen related growth factors in the genome of	
A;Reference number: Z20880; PMID:99148833	
A;Accession: T30807	
A;Status: preliminary; translated from GB/EMBL/DDJB	
A;Molecule type: DNA	
A;Residues: 1-433 <COT>	
A;Cross-references: EMBL:AJ010317; NID:e1355235; PID:e1355237; PIDN:CAA090844	
C;Genetics:	
A;Gene: TRIP	
A;Introns: 33/2; 52/3; 80/3; 94/1; 136/3; 168/2; 206/2; 235/3; 265/3; 310/1; 352/3; 3	

Query Match Best Local Similarity 83.3%; Pred. No. 2e-21; DB 2; Length 433; Matches 39; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CTCICSDFFDHSDVAIHCQHPTFLQLQIQLWETAPSRTCPQCRLQVG 50

Db 7 CTCICSDFFDHSDVAIHCQHPTFLQLQIQLWETAPSRTCPQCRLQVG 53

RESULT 2

C84701 hypothetical protein At2g29840 [imported] - Arabidopsis thaliana (mouse-ear cress)

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: C84701

R;Liin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.C.D.; Fujii, C.Y.

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; PMID:20083487

A;Accession: C84701

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-310 <STO>

A;Cross-references: GB:AE002093; NID:g3582320; PIDN: AAC35217.1; GSDB:GN00139

C;Genetics:

A;Gene: At2g29840

A;Map position: 2

ALIGNMENTS

30	98	33.4	343	2	H96703	probable RING zinc
31	97.5	33.3	257	2	T48058	RING-H2 zinc finger
32	97	33.3	211	2	F8488	protein T33E20.33
33	97	33.1	235	2	T19322	hypothetical prote
34	97	33.1	407	2	G98335	probable RING zinc
35	96.5	32.9	194	2	C81130	hypothetical prote
36	96.5	32.9	203	2	T48129	probable zinc finger
37	96.5	32.9	304	2	T52079	hypothetical prote
38	96.5	32.9	408	2	T25224	unknown protein, 8
39	96	32.8	145	2	B96705	hypothetical prote
40	96	32.8	377	2	T26958	hypothetical prote
41	96	32.8	488	2	T10675	hypothetical prote
42	96	32.8	530	2	T50499	probable RING zinc
43	95.5	32.6	162	2	E84555	hypothetical prote
44	95	32.4	189	2	T05383	hypothetical prote
45	95	32.4	238	2	T49155	hypothetical prote

Query Match

Score 43.3%;

DB 2;

Length 310;

Matches	20;	Conservative	41.7%;	Pred.	No.	1.1e-07;	Mismatches	11;	Indels
Qy	3	LCTICSDDEFDHRSRVAIHCQHTFHQLCQILOWFETAPSRTCPQCRIQV	50					2;	Caps
Db	260	MCSCLEFFDGRSIVALPGHEFDDECAKWFET-NHDCPLCRFKL	305					1;	
RESULT	3								
R6A14.12	protein - Arabidopsis thaliana (mouse-ear cress)								
C;Species:	Arabidopsis thaliana (mouse-ear cress)								
C;Date:	02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Nov-2001								
C;Accession:	R86321								
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.H.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, R.; ansen, N.F.; Hughes, B.; Huizar, L.									
Nature	408,	816-820,	2000						
A;Authors:	Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.								
A;Authors:	Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.								
A;Title:	Sequence and analysis of chromosome 1 of the plant Arabidopsis.								
A;Reference number:	A86141; MUID:21016719								
A;Accession:	R86321								
A;Status: preliminary									
A;Molecule type: DNA									
A;Residues: 1-325 <STO>									
A;Cross-references:	GB:AE005172; PIDN:AAF27102.1; GSPDB:GN00141								
C;Genetics:									
A;Map position:	1								
RESULT	4								
Query Match	42.7%	Score	125;	DB	2;	Length	325;		
Best Local Similarity	39.6%	Pred.	No.	2e-07;					
Matches	19;	Conservative	11;	Mismatches	16;	Indels	2;	Gaps	1;
Qy	3	LCTICSDDEFDHRSRVAIHCQHTFHQLCQILOWFETAPSRTCPQCRIQV	50						
Db	276	VCTICLEEFDGSRIVTLPQGHEFDDECVLWEP--VRSHVCPCLRL	321						
RESULT	4								
Query Match	42.7%	Score	125;	DB	2;	Length	325;		
Best Local Similarity	39.6%	Pred.	No.	2e-07;					
Matches	19;	Conservative	11;	Mismatches	16;	Indels	2;	Gaps	1;
Qy	3	LCTICSDDEFDHRSRVAIHCQHTFHQLCQILOWFETAPSRTCPQCRIQV	50						
Db	276	VCTICLEEFDGSRIVTLPQGHEFDDECVLWEP--VRSHVCPCLRL	321						
RESULT	6								
Query Match	38.6%	Score	113;	DB	2;	Length	224;		
Best Local Similarity	40.4%	Pred.	No.	3.9e-06;					
Matches	19;	Conservative	9;	Mismatches	17;	Indels	2;	Gaps	1;
Qy	4	CTICSDDEFDHRSRVAIHCQHTFHQLCQILOWFETAPSRTCPQCRIQV	50						
Db	175	CTICLLEEFNDGTKVMTLPQGHEFDDECVLWEP--NHDCPLCRFKL	219						
RESULT	6								
Query Match	38.6%	Score	113;	DB	2;	Length	224;		
Best Local Similarity	40.4%	Pred.	No.	3.9e-06;					
Matches	19;	Conservative	9;	Mismatches	17;	Indels	2;	Gaps	1;
Qy	4	CTICSDDEFDHRSRVAIHCQHTFHQLCQILOWFETAPSRTCPQCRIQV	50						
Db	175	CTICLLEEFNDGTKVMTLPQGHEFDDECVLWEP--NHDCPLCRFKL	219						
RESULT	6								
Query Match	38.6%	Score	113;	DB	2;	Length	224;		
Best Local Similarity	40.4%	Pred.	No.	3.9e-06;					
Matches	19;	Conservative	9;	Mismatches	17;	Indels	2;	Gaps	1;
Qy	4	CTICSDDEFDHRSRVAIHCQHTFHQLCQILOWFETAPSRTCPQCRIQV	50						
Db	175	CTICLLEEFNDGTKVMTLPQGHEFDDECVLWEP--NHDCPLCRFKL	219						
RESULT	6								
Query Match	38.6%	Score	113;	DB	2;	Length	224;		
Best Local Similarity	40.4%	Pred.	No.	3.9e-06;					
Matches	19;	Conservative	9;	Mismatches	17;	Indels	2;	Gaps	1;
Qy	4	CTICSDDEFDHRSRVAIHCQHTFHQLCQILOWFETAPSRTCPQCRIQV	50						
Db	175	CTICLLEEFNDGTKVMTLPQGHEFDDECVLWEP--NHDCPLCRFKL	219						
RESULT	7								
Query Match	38.2%	Score	112;	DB	2;	Length	344;		
Best Local Similarity	38.3%	Pred.	No.	7.3e-06;					
Matches	18;	Conservative	9;	Mismatches	18;	Indels	2;	Gaps	1;
Qy	4	CTICSDDEFDHRSRVAIHCQHTFHQLCQILOWFETAPSRTCPQCRIQV	50						
Db	229	CTICLLEEFNDGTKVMTLPQGHEFDDECVLWEP--CPVCRYEL	273						

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Fedderspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, D.; Conway, A.R.; Creasy, T.H.; Dewar, K.; antis, N.F.; Hughes, B.; Huijar, L.; Nature, 408, 816-820, 2000
 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Selzberg, S.I.; Schwartz, J.R.; Shin, P.; Southwick, A.M.; Veitler, J.C.; Davis, R.W.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, R.W.; A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A;Reference number: A86315; MUID:21016719
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-383 <STO>
 A;Cross-references: GB:AE005172; NID:99665074; PIDN:AAF97276.1; GSPDB:GN00141
 C;Genetics:
 A;Map position: 1

Query Match 38.2%; Score 112; DB 2; Length 383;
 Best local Similarity 36.4%; Pred. No 8e-06; Mismatches 16; Conservative 11; Indels 2; Gaps 1;
 Matches 15; C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
 C;Accession: T48296
 R;Baev, M.; Terryn, N.; Arribalzaga, W.; Buysehaert, C.; Dasseville, R.; De Clerck, R.; De ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.
 submitted to the Protein Sequence Database, April 2000
 A;Reference number: Z24491
 A;Accession: T48296
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-274 <BEV>
 A;Cross-references: EMBL:AL162973
 A;Experimental source: cultivar Columbia; BAC clone F9G14
 C;Genetics:
 A;Map position: 5
 A;Note: F9G14_60
 C;Superfamily: RING finger homology homology <RRN>
 F;81-131/Domain: RING finger homology <RRN>
 F;201-251/Domain: RING finger homology <RRN>

RESULT 8
 T48296
 hypothetical protein F9G14_60 - Arabidopsis thaliana
 C;Species: Homo sapiens (man)
 C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 02-Sep-2000
 C;Accession: T46904
 A;Experimental source: adult amygdala; submitted to the Protein Sequence Database, February 2000
 A;Reference number: Z24496
 A;Accession: T46904
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-137 <AAA>
 A;Cross-references: EMBL:AL157474
 A;Experimental source: adult amygdala;
 C;Genetics:
 A;Note: DKFZP761D081.1
 C;Superfamily: RING finger homology homology <RRN>
 F;81-131/Domain: RING finger homology <RRN>

Query Match 36.5%; Score 107; DB 2; Length 137;
 Best local Similarity 38.3%; Pred. No. 1e-05; Mismatches 18; Conservative 7; Indels 2; Gaps 1;
 Matches 20; C;Species: Saccharomyces cerevisiae
 C;Alternate names: hypothetical protein 02341
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
 C;Accession: T26069
 R;White, S.
 submitted to the EMBL Data Library, November 1996
 A;Accession number: Z20147
 A;Reference number: T26069
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-489 <WIL>
 A;Cross-references: EMBL:ZB02062; PIDN:CA04890.1; GSPDB:GN00019; CESP:W02A11.3
 A;Experimental source: clone W02A11
 C;Genetics:
 A;Gene: CESP:W02A11.3
 A;Map position: 1
 A;Introns: 58/3; 129/3; 361/3; 444/3
 C;Superfamily: RING finger homology homology <RRN>
 F;429-479/Domain: RING finger homology homology <RRN>

Query Match 36.9%; Score 108; DB 2; Length 489;
 Best local Similarity 29.8%; Pred. No. 2.9e-05; Mismatches 14; Conservative 12; Indels 2; Gaps 1;
 Matches 19; C;Species: Homo sapiens (man)
 C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 02-Sep-2000
 C;Accession: T46904
 A;Experimental source: adult amygdala; submitted to the Protein Sequence Database, February 2000
 A;Reference number: Z24496
 A;Accession: T46904
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-137 <AAA>
 A;Cross-references: EMBL:AL157474
 A;Experimental source: adult amygdala;
 C;Genetics:
 A;Note: DKFZP761D081.1
 C;Superfamily: RING finger homology homology <RRN>
 F;81-131/Domain: RING finger homology <RRN>

RESULT 9
 T26069
 hypothetical protein W02A11_3 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
 C;Accession: T26069
 R;White, S.
 submitted to the EMBL Data Library, November 1996
 A;Accession number: Z20147
 A;Reference number: T26069
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-551 <HUG>
 A;Cross-references: EMBL:Z74755; NID:91419784; PID:e252259; PID:g141985; MIPS:YOL013C
 A;Experimental source: strain S288C
 C;Genetics:
 A;Gene: SGD:HRD1
 A;Cross-references: SGD:S0005373; MIPS:YOL013C
 A;Map position: 15L
 C;Superfamily: RING finger homology homology <RRN>
 C;Keywords: transmembrane protein
 F;46-62/Domain: transmembrane #status predicted <TM1>
 F;46-62/Domain: transmembrane #status predicted <TM2>

Query Match	Score	DB	Length	Matches	Conservative	Mismatches	Indels	Gaps	1;
F;05-121/Domain: transmembrane #status predicted <TM3> F;14-160/Domain: transmembrane #status predicted <TM4> F;345-405/Domain: RING finger homology <RRN>									
Query Match	36.5%	Score 107;	DB 2;	Length 551;					
Best Local Similarity	37.3%	Pred. No.	4.3e-05;	Indels	2;	Gaps	2;		
Matches	22;	Conservative	6;	Mismatches	19;				
Qy	2	SLC11CSDFPFDHS-----	RDVAIHCIGTFHLOCLIONFETAPSRTCPQRIOV	50					
Db	347	NCICICMDELHSPNQQTWKNNKKPKRLLPCGHLHLISCLKNMNER-SQTCPICRPV	403						
RESULT 12									
F85016		probable RING zinc finger protein [imported] - Arabidopsis thaliana							
C;Species: Arabidopsis thaliana (mouse-ear cress)									
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001									
C;Accession: F85016									
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999									
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.									
A;Reference number: A85001; MUID: 20083488									
A;Accession: F85016									
A;Status: preliminary									
A;Molecule type: DNA									
A;Residues: 1-506 <STO>									
A;Cross-references: GB:NC_001268; NID:97267624; PIDN:CAF80936.1; GSPDB:GN00140									
C;Genetics:									
A;Gene: AT4g01270									
A;Map position: 4									
Query Match	36.3%	Score 106.5;	DB	2;	Length 506;				
Best Local Similarity	39.6%	Pred. No.	4.5e-05;	Indels	10;	Mismatches	13;	Gaps	2;
Matches	21;	Conservative	10;						
Qy	2	SLC11CSDFPFDHS-----	RDVAIHCIGTFHLOCLIONFETAPSRTCPQRIOV	47					
Db	10	AIKSCICYEDLKPVENLQSIKA-CGHFHELCLQWFEYCUDSTNKRNCPICK	60						
RESULT 13									
H95764		protein RING zinc finger protein F25P22.18 [imported] - Arabidopsis thaliana (mouse-ear cress)							
C;Species: Arabidopsis thaliana (mouse-ear cress)									
C;Accession: H95764									
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001									
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Hulzar, L.									
Nature 408, 816-820, 2000									
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziali, A.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.; Talloker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.									
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.									
A;Reference number: A86141; MUID: 21016719									
A;Status: preliminary									
A;Molecule type: DNA									
A;Residues: 1-367 <STO>									
A;Cross-references: GB:AE005173; NID:96692739; PIDN:AAF24845.1; GSPDB:GN00141									
C;Genetics:									
A;Gene: F25P22.18									
A;Map position: 1									
Query Match	36.2%	Score 106;	DB	2;	Length 524;				
Best Local Similarity	36.4%	Pred. No.	4e-05;	Indels	2;	Mismatches	1;	Gaps	1;
Matches	16;	Conservative	8;						
Qy	4	CTTCSDFFDHSRVAATHCIGTFHLOCLIONFETAPSRTCPQRIOV	47						
Db	319	CTICQDEYEAKDEVGEILRGHRFHIDCVNNQWL-VRKNSCPCK	360						
RESULT 14									
T22457		hypothetical protein B0432.9 - Caenorhabditis elegans							
C;Species: Caenorhabditis elegans									
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000									
R;Henkhaus, J.; Wohlmann, P.									
submitted to the EMBL Data Library, December 1996									
A;Description: The sequence of C. elegans cosmid B0432.									
A;Reference number: T220038									
A;Accession: T225457									
A;Status: preliminary; translated from GB/EMBL/DDJB									
A;Molecule type: DNA									
A;Residues: 1-425 <HEN>									
A;Cross-references: EMBL:UB0836; PIDN:AB37893.1; GSPDB:GN00020; CESP:B0432.9									
A;Experimental source: strain Bristol N2; clone B0432									
A;Gene: CESP:B0432.9									
A;Map position: 2									
A;Introns: 64/3; 99/3; 165/1; 267/3; 350/2; 386/2									
C;Superfamily: RING finger homology									
F;188-238/Domain: RING finger homology <RRN>									
Query Match	36.2%	Score 106;	DB	2;	Length 425;				
Best Local Similarity	40.9%	Pred. No.	4.5e-05;	Indels	2;	Mismatches	17;	Gaps	1;
Matches	18;	Conservative	7;						
Qy	4	CTTCSDFFDHSRVAATHCIGTFHLOCLIONFETAPSRTCPQRIOV	47						
Db	192	CSICFEDLKDQNDKISAIVCIGHYHGCISQIAT-KRCPCSCR	233						
RESULT 15									
F9572		protein F12M16.10 [imported] - Arabidopsis thaliana							
C;Species: Arabidopsis thaliana (mouse-ear cress)									
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001									
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Hulzar, L.									
Nature 408, 816-820, 2000									
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziali, A.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.; Talloker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.									
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.									
A;Reference number: A86141; MUID: 21016719									
A;Status: preliminary									
A;Molecule type: DNA									
A;Residues: 1-524 <STO>									
A;Cross-references: GB:AE005173; NID:97769853; PIDN:AAF69531.1; GSPDB:GN00141									
C;Genetics:									
A;Gene: F12M16.10									
A;Map position: 1									
Query Match	36.2%	Score 106;	DB	2;	Length 524;				
Best Local Similarity	36.4%	Pred. No.	4e-05;	Indels	2;	Mismatches	1;	Gaps	1;
Matches	16;	Conservative	8;						
Qy	4	CTTCSDFFDHSRVAATHCIGTFHLOCLIONFETAPSRTCPQRIOV	47						

Db 472 CTICQESPKNEEKIATIDCGHEWHAECLEKWL-IVKNVCPICK 513

hypothetical protein T5A14.7 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change.31-Mar-2001

C;Accession: F96597

R;Theologis, A.; Ecker, J.R.; Fedderspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Species: *Caenorhabditis elegans*

C;Accession: T15919

T15919 hypothetical protein EEDB8.9 - *Caenorhabditis elegans*

C;Accession: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 02-Sep-2000

C;Accession: T15919

R;Chissoe, S.; submitted to the EMBL Data Library, July 1995

A;Description: The sequence of *C. elegans* cosmid EEDB8.

A;Reference number: 218428

A;Accession: T15919

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: I-1238 <CHT>

A;Experimental source: strain Bristol N2

A;Cross-references: EMBL:U23484; NID:9733597; PID:9733606; PIDN:AAC46769_1; CESP:EEDB8.9

C;Genetics: CESP:EEDB8.9

A;Introns: 15/3; 60/3; 140/1; 192/3; 269/2; 402/2; 637/3; 717/3; 769/1; 855/3; 888/3; 10

C;Superfamily: RING finger homology

F:9594-950/Domain: RING finger homology <RRN>

RESULT 17

F71425 Query Match 35.8%; Score 105; DB 2; Length 1238; Best Local Similarity 44.7%; Pred. No. 0.00015; Matches 21; Conservative 5; Mismatches 15; Indels 6; Gaps 2; Db 905 LPPCAVCLERMDSS--VLAILCHNSFHARCLEWAD--NTCPVCR 945

RESULT 17

F71425 hypothetical protein - *Arabidopsis thaliana*

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

A;Variety: columbia

C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 02-Sep-2000

C;Accession: F71425

R;Jeevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk P.; Wedler, H.; Wedler, R.; Wambutt, R.; Weitzneger, T.; Poll, T.M.; Terryn, N.; Gien avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.

Nature 391, 485-488, 1998

A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech, R.; erhoff, A.; Moores, T.; Jones, J.D.G.; Envera, T.; Palme, K.; Bene, P.; Rechman, S.; Ans

C.; Chalwatzis, N.

A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of *Arabidopsis thal*

A;Reference number: A71400; MUID:98121113

A;Accession: F71425

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: I-441 <BEV>

A;Cross-references: GB:Z97340; NID:92244950; PID:e326963; PID:92244955

C;Genetics:

A;Map position: 4COP9-G3845

C;Superfamily: RING finger homology

F:278-329/Domain: RING finger homology <RRN>

RESULT 19

G84678 Query Match 35.5%; Score 104; DB 2; Length 351; Best Local Similarity 38.3%; Pred. No. 6.6e-05; Matches 18; Conservative 7; Mismatches 20; Indels 2; Gaps 1; Db 223 CSVCLDDDFEIGTEAKLMPCTHKFHSDCCLPWLHSS--CPVCRYQL 267

RESULT 19

G84678 probable RING zinc finger protein [imported] - *Arabidopsis thaliana*

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: G84678

R;Jin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y

R;Jin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y

R;Jin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y

R;Jin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y

R;Jin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y

R;Jin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y

R;Jin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y

R;Jin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y

R;Jin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y

R;Jin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y

R;Jin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y

R;Jin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y

R;Jin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y

RESULT 20

T51859 Query Match 35.0%; Score 102.5; DB 2; Length 237; Best Local Similarity 42.2%; Pred. No. 7.1e-05; Matches 19; Conservative 4; Mismatches 19; Indels 3; Gaps 2; Db 140 CVICLSDFFEEGETVKVPHCIVHVDVDTWLSSVV--TCPLCR 182

RESULT 20

T51859 probable RING finger protein RHG1a [imported] - *Arabidopsis thaliana* (fragment)

C;Species: *Arabidopsis thaliana* (mouse-ear cress)

C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000

C;Accession: T51859

R;Jensen, R.B.; Jensen, K.L.; Jespersen, H.M.; Skriver, K.

FEBS Lett. 436, 283-7, 1998

RESULT 18

F9597

A;Title: Widespread occurrence of a highly conserved RING-H2 zinc finger motif in the mouse genome
A;Reference number: Z13771; MUID:98452956
A;Accession: T51859
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Residues: 1-190 <JEN>
A;Cross-references: EMBL:AF079183; PIDN: AAC69857.1

RESULT 21
Query Match 34.8%; Score 102; DB 2; Length 190;
Best Local Similarity 31.8%; Pred. No. 6.7e-05;
Matches 14; Conservative 9; Mismatches 19; Indels 2; Gaps 1;
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 02-sep-2000
C;Accession: T06684
R;Quetier, F.; Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artigau, E.; Reference number: 215793
A;Accession: T06684
A;Molecule type: DNA
A;Residues: 1-292 <QER>
A;Cross-references: EMBL:AL049658; GSPDB:GN00061; ATSP:T17F15.140
A;Experimental source: cultivar Columbia; BAC clone T17F15
C;Genetics:
A;Gene: ATSP:T17F15.140
A;Introns: 37/3; 68/3; 90/3; 143/3; 181/3
C;Superfamily: RING finger homology
A;Domain: RING finger homology <RRN>
F;165-215/Domain: RING finger homology <RRN>

RESULT 22
Query Match 34.8%; Score 102; DB 2; Length 292;
Best Local Similarity 36.2%; Pred. No. 9.7e-05;
Matches 17; Conservative 8; Mismatches 20; Indels 2; Gaps 1;
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T51849
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
A;Accession: A84420
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-425 <STO>
A;Cross-references: GB:AE002093; NID:91871181; PIDN: AAB63541.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g2030
A;Map position: 2

Query Match 34.6%; Score 101.5; DB 2; Length 425;
Best Local Similarity 36.2%; Pred. No. 0.00015;

RESULT 23
Query Match 34.8%; Score 102; DB 2; Length 157;
Best Local Similarity 34.3%; Pred. No. 8.6e-05;
Matches 19; Conservative 4; Mismatches 21; Indels 1; Gaps 1;
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 02-Sep-2000
C;Accession: T13027
R;Bevan, M.; Peters, S.A.; van Slaveren, M.; Dirks, W.; Stiekema, W.; Bancroft, I.; submitted to the Protein Sequence Database, July 1999
A;Reference number: 217587
A;Accession: T13027
A;Molecule type: DNA
A;Residues: 1-157 <BEV>
A;Cross-references: EMBL:AL096882; GSPDB:GN00062; ATSP:F8L21.150
A;Experimental source: cultivar Columbia; BAC clone F8L21
C;Genetics:
A;Gene: ATSP:F8L21.150
A;Map position: 4
C;Superfamily: RING finger homology
F;81-134/Domain: RING finger homology <RRN>

RESULT 24
Query Match 34.3%; Score 100.5; DB 2; Length 157;
Best Local Similarity 42.2%; Pred. No. 8.6e-05;
Matches 19; Conservative 4; Mismatches 21; Indels 1; Gaps 1;
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T51841
R;Jensen, R.B.; Jensen, K.L.; Jespersen, H.M.; Skriver, K.
FEBS Lett. 436, 203-7, 1998
A;Title: Widespread occurrence of a highly conserved RING-H2 zinc finger motif in the mouse genome
A;Reference number: Z13771; MUID:98452956
A;Accession: T51841
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Cross-references: EMBL:AF078821; PIDN: AAC68670.1
A;Experimental source: cultivar Columbia

RESULT 25
Query Match 34.3%; Score 100.5; DB 2; Length 157;
Best Local Similarity 42.2%; Pred. No. 8.6e-05;
Matches 19; Conservative 4; Mismatches 21; Indels 1; Gaps 1;
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001
C;Accession: C85067
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999

A;Title: Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana*.
A;Reference number: AB5001; MUID: 20083488
A;Accession: C85067
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-206 <STO>
A;Cross-references: GB:NC_001268; NID:97267295; PIDN:CAB81077.1; GSPDB:GN00140
C;Genetics:
A;Gene: AT4g05350
A;Map position: 4
C;Superfamily: *Arabidopsis thaliana* hypothetical RING finger protein F16J13.210; RING fi

Query Match 34.0%; Score 99.5; DB 2; Length 206;
Best Local Similarity 36.0%; Pred. No. 0.00014; Matches 18; Conservative 8; Mismatches 19; Indels 5; Gaps 2;

Qy 4 CTICSDFF--DHSRDVAIHCQHTFHQLQIOWFETAPSRSRCPQCRIQV 50
Db 157 CSICLESLVSGPKPRDVTRMTCSHVFHNGCLLWLRK--KNTCPLCRTE 204

RESULT 26

T11681 hypothetical protein SPBC21D10.09c - fission yeast (*Schizosaccharomyces pombe*)
C;Species: *Schizosaccharomyces pombe*
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 02-Sep-2000
C;Accession: T11681
R;Seeger, K.; Harris, D.; Wood, V.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1998
A;Reference number: Z17313
A;Accession: T11681
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-1610 <SEE>
A;Cross-references: EMBL:AL031536; NID:e1319499; PID:e1319508
A;Experimental source: strain 92h(-)
C;Genetics:
A;Map position: IIR
A;Introns: 10/2
A;Note: SPBC21D10.09c
C;Superfamily: RING finger homology <RRN>
F1554-1609/Domain: RING finger homology <RRN>

Query Match 34.0%; Score 99.5; DB 2; Length 1610;
Best Local Similarity 38.3%; Pred. No. 0.00082; Matches 18; Conservative 5; Mismatches 21; Indels 3; Gaps 1;

Qy 4 CTICSDFFDHRSRVAATGCG--HTFHQCLQIOWFETAPSRSRCPQCRIQV 47
Db 1558 CAICYSVLSVERTLPNKRKGTCRHKFHASCLYKWFKSSNSRCPLCR 1604

RESULT 27

T00428 hypothetical protein At2g47560 [imported] - *Arabidopsis thaliana*
N;Alternative names: hypothetical protein T30B22.14
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 16-Feb-2001
C;Accession: T00428; G84916
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Masc
submitted to the EMBL Data Library, October 1998 BAC T30B22 genomic sequence.
A;Description: *Arabidopsis thaliana* chromosome II BAC T30B22 genomic sequence.
A;Reference number: Z14149
A;Accession: T00428
A;Status: translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-227 <ROU>
A;Cross-references: EMBL:AC002535; NID:92529657; PID:92529671

Query Match 34.0%; Score 99.5; DB 2; Length 1610;
Best Local Similarity 38.3%; Pred. No. 0.00082; Matches 18; Conservative 5; Mismatches 21; Indels 3; Gaps 1;

Qy 4 CTICSDFFDHRSRVAATGCG--HTFHQCLQIOWFETAPSRSRCPQCRIQV 47
Db 1558 CAICYSVLSVERTLPNKRKGTCRHKFHASCLYKWFKSSNSRCPLCR 1604

RESULT 28

G84530 probable RING-H2 zinc finger protein [imported] - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: G84530
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A;Reference number: A84420; MUID:20083487
A;Accession: G84530
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: GB:AE002093; NID:94335724; PIDN:AD17402.1; GSPDB:GN00139
C;Genetics:
A;Gene: At2g15580
A;Map position: 2

Query Match 33.4%; Score 98; DB 2; Length 204;
Best Local Similarity 36.2%; Pred. No. 0.00021; Matches 17; Conservative 6; Mismatches 22; Indels 2; Gaps 1;

Qy 4 CTICSDFFDHRSRVAATGCG--HTFHQCLQIOWFETAPSRSRCPQCRIQV 50
Db 158 CAICIDRFFKGETLVHLPCAHKFHSICLLPWLDT--NVCPYCRTDI 202

RESULT 29

E84918 hypothetical protein At2g47700 [imported] - *Arabidopsis thaliana*
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: E84918
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
A;Reference number: A84420; MUID:20083487
A;Accession: E84918
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-324 <DNA>
A;Cross-references: GB:AB002093; NID:93738284; PIDN: AAC63626.1; GSPDB:GN00139

C;Genetics:
A;Gene: At2g47700
A;Map position: 2

Query Match 33.4%; Score 98; DB 2; Length 324;
Best Local Similarity 41.3%; Pred. No. 0.00032; Matches 19; Conservative 5; Mismatches 20; Indels 2; Gaps 1;

Qy 4 CTIC--SDFDFHSRVAATIHCGLTFLHQCLIQWETAPSRTPQCPCR 47
Db 38 CSICLESVLDGDTUSKAKLQCGHOPFLDQIGSAFNNKGAMQCPCPR 83

RESULT 30

H96703 probable RING zinc finger protein T23K23.8 [imported] - Arabidopsis thaliana (mouse-ear cress)

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: H96703
C;Theology: A.; Ecker, J.R.; Palm, C.J.; Fedderspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talloker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: H96703
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-343 <STO>
A;Cross-references: GB:AE005173; NID:96553869; PIDN:AAF16555.1; GSPDB:GN00141
A;Genetics:
A;Gene: T23K23.8
A;Map position: 1

Query Match 33.4%; Score 98; DB 2; Length 343;
Best Local Similarity 27.7%; Pred. No. 0.00033; Matches 13; Conservative 19; Indels 2; Gaps 1;

Qy 4 CTICSDFFDHSHRVAATIHCGLTFLHQCLIQWETAPSRTPQCPCR 50
Db 292 CCCCLSLSTEDGAELVSLPONHNHFHSTCTVWLKM-NATCPLRKFNT 336

RESULT 31

T48058 RING-H2 zinc finger protein ATI5 - Arabidopsis thaliana
N;Alternate names: protein F26K9_120
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: T48058
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 08-Dec-2000
C;Accession: T48058
C;Accession: Meves, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X.; Quetier, F.; Salanouba submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24465
A;Accession: T48058
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-257 <BL0>
A;Cross-references: EMBL:ALI62651
A;Experimental source: cultivar Columbia; BAC clone F26K9
C;Genetics:
A;Map position: 3
A;Note: F26K9_120
C;Superfamily: Arabidopsis hypothetical protein F19I3.22; RING finger homology <RRN>
F109-160/Domain: RING finger homology <RRN>

Query Match 33.3%; Score 97; DB 2; Length 257;
Best Local Similarity 37.3%; Pred. No. 0.0003; Matches 19; Conservative 7; Mismatches 22; Indels 3; Gaps 2;

Qy 1 LSLCTIC-SDFDFHSRVAATIHCGLTFLHQCLIQWETAPSRTPQCPCR 50
Db 110 LEECSVCLSEFEDEDEGRVLVLPKCGHVFDIDTWFRSSS--CPLCRAPV 158

RESULT 32

F86488 protein T33E20.33 [imported] - Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Accession: F86488
C;Theology: A.; Ecker, J.R.; Palm, C.J.; Fedderspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Talloker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: H96703
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-211 <STO>
A;Cross-references: GB:AE005172; NID:98778785; PIDN:AAF79793.1; GSPDB:GN00141
A;Genetics:
A;Gene: T32E20.33
A;Map position: 1

Query Match 33.1%; Score 97; DB 2; Length 211;
Best Local Similarity 35.6%; Pred. No. 0.00029; Matches 16; Conservative 7; Mismatches 20; Indels 2; Gaps 1;

Qy 3 LCTICSDFFDHSHRVAATIHCGLTFLHQCLIQWETAPSRTPQCPCR 47
Db 85 ICCICQDRQRAGVGKLNCGHNFHINSVKPWILT-KKQCPVCQ 127

RESULT 33

T19328 hypothetical protein C16C10.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Accession: T19328
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
C;Accession: T19328
C;Reference number: Z19108
A;Accession: T19328
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-235 <WIL>
A;Cross-references: EMBL:Z46787; PIDN:CAA86745.1; GSPDB:GN00021; CESP:C16C10.7
A;Experimental source: clone C16C10
C;Genetics:
A;Gene: CESP:C16C10.7
A;Map position: 3
A;Introns: 23/2; 105/3; 196/1
C;Superfamily: RING finger homology <RRN>
F22-72/Domain: RING finger homology <RRN>

Query Match 33.1%; Score 97; DB 2; Length 235;
Best Local Similarity 40.0%; Pred. No. 0.00032; Matches 18; Conservative 6; Mismatches 17; Indels 4; Gaps 2;

Qy 4 CTICSDFFDHSHRVAATIHCGLTFLHQCLIQWETAPSRTPQCPCR 47

RESULT 34
DB 26 CNIC--LDAKDAVSLCGLFCWPCLSQWLDRPNNQVCPCVK 67

G96835 probable RING zinc finger protein, 53384-54880 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: G96835
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Fedderspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chung, M.K.; Conn, L.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.F.; Hughes, B.; Hultzar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lurco, J.S.; Maiti, R.; Marzali, R.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.; Residues: 1-407 <STO>
A;Cross-references: GB:AE005173; NID:96751714; PIDN:AAF27696.1; GSPDB:GN00141
A;Genetics:
A;Gene: F5I6.15
A;Map position: 1

RESULT 35
C85130 hypothetical protein At4g12190 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Mar-2001
C;Accession: C85130
R;Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID: 20083488
A;Accession: C85130
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-194 <STO>
A;Cross-references: GB:NC_001268; NID:97267920; PIDN:CABT8262.1; GSPDB:GN00140
C;Genetics:
C;Gene: At4g12190
A;Map position: 4
C;Superfamily: Arabidopsis thaliana hypothetical RING finger protein F16J13.210; RING f1

Query Match 32.9%; Score 96.5; DB 2; Length 194;
Best Local Similarity 34.0%; Pred. No. 0.00031; Matches 17; Conservative 9; Mismatches 19; Indels 5; Gaps 2;
Oy 4 CTICSDFFDHSDRVAAI-HCCHTFHQCLQFETAPSRTCPQCRCQV 50
Db 355 CCICLTRYGDDEQRELPCHVFRHVCDVWLKR--NATCPLCKNEVG 400

RESULT 36
T48129 hypothetical protein T4C9.30 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 18-Aug-2000
C;Accession: T48129
R;Beraa, M.; Peters, S.A.; van Staeren, M.; Dirks, W.; Stiekema, W.; Bancroft, I.; submitted to the Protein Sequence Database, June 1999
A;Reference number: Z24485
A;Accession: T48129
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-203 <BEV>
A;Cross-references: EMBL:AL080318
A;Experimental source: cultivar Columbia; BAC clone T4C9
C;Genetics:
A;Map position: 4
A;Introns: 9/3
A;Note: T4C9.30
C;Superfamily: Arabidopsis thaliana hypothetical RING finger homology <RRN> F150-203/Domain: RING finger homology <RRN>
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID: 21016719
A;Accession: G96835
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-407 <STO>
A;Cross-references: GB:AE005173; NID:96751714; PIDN:AAF27696.1; GSPDB:GN00141
A;Gene: F5I6.15
A;Map position: 1

RESULT 37
T52079 probable zinc finger protein [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 20-Oct-2000
C;Accession: T52079
R;Martinezgarcia, M.; Garciduenas, C.; Guzman, P.
Mol. Gen. Genet. 252, 587-596, 1996
A;Title: Gene isolation in arabidopsis-thaliana by conditional overexpression of cdn
A;Reference number: Z04056
A;Accession: T52079
A;Status: preliminary
A;Molecule type: translated from GB/EMBL/DDJB
A;Residues: 1-304 <MAR>
A;Cross-references: EMBL:L76926; PIDN: AAC77829.1

RESULT 38
T25524 hypothetical protein C06A5.9 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T25524
R;Davidson, S.; Wohldmann, P.
submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosmid C06A5.
A;Reference number: Z20044
A;Accession: T25524
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: DNA
A;Residues: 1-408 <DAV>
A;Cross-references: EMBL:U97193; PIDN: AAB52442.1; GSPDB: GN00019; CESP:C06A5.9
C;Genetics:
A;Gene: CESP:C06A5.9

A; Map position: 1 A; Introns: 3/1; 27/3; 86/1; 154/1; 201/3; 240/3; 268/3; 297/3	Query Match Best Local Similarity 32.9%; Score 96.5; DB 2; Length 408; Matches 17; Conservative 12; Mismatches 17; Indels 3; Gaps 2;
OY Db	4 CTICSDFDDHSRDA-AIHCGHTFHLOCL--TOWFETAPSRCPOCRIQ 49 22 CQVCYQPFFNETKLARSLHCGHTFCCTECIRNWNQNGNSPHLECPTCRAE 70
RESULT 39	
B96705	unknown protein, 88740-88303 [imported] - Arabidopsis thaliana
C; Species: Arabidopsis thaliana (mouse-ear cress)	
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001	
C; Accession: B96705	
R; Theologis, A.; Ecker, J.R.; Palm, C.J.; Fedderspiel, N.A.; Kaul, S.; White, O.; A. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.	
Nature 408, 816-820, 2000	
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; K. C.A., Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luro, J.S.; Mati, R.; Marr, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.	
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Barker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.	
A; Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.	
A; Reference number: A86141; MUID:21016719	
A; Accession: B96705	
A; Status: preliminary	
A; Molecule type: DNA	
A; Residues: 1-145 <STO>	
A; Cross-references: GB:AE005173; NID:9615736; PIDN:AAF26497.1; GSPDB:GN00141	
A; Genetics:	
A; Gene: T22E19.19	
A; Map position: 1	
RESULT 40	
T26958	Query Match 32.8%; Score 96; DB 2; Length 145;
hypothetical protein Y47D3B.11 - Caenorhabditis elegans	
C; Species: Caenorhabditis elegans	
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000	
C; Accession: T26958	
R; Matthews, L.	
submitted to the EMBL Data Library, September 1998	
A; Reference number: Z22090	
A; Accession: T26958	
A; Status: preliminary; translated from GB/EMBL/DDBJ	
A; Molecule type: DNA	
A; Residues: 1-377 <NTL>	
A; Introns: 52/1; 81/3; 152/3	
A; Cross-references: EMBL:AL031635; PIDN:CAB54384.1; GSPDB:GN00021; CESP:Y47D3B.11	
A; Experimental source: clone Y47D3B	
C; Genetics:	
A; Gene: CESP:Y47D3B.11	
A; Map position: 3	
A; Superfamily: RING finger homology	
C; Superfamily: RING finger homology <RRN>	
F; 313-363/Domain: RING finger homology <RRN>	

Qy	Best Local Similarity	Local Similarity	Pred.	No.	Mismatches	Indels	Gaps	1:
Db	4	CTICSDFFHDHSRDAVAAHGCHGTFHLOCLLQRNRETAPSRTCPORIOV	: : : : : : : : : : :	50				
	317	CVICLEEVEGTELRLFCGHFHPKCVDPWL-LSKRRRCPLCQFDV	361					

Search completed: September 4, 2002, 16:13:07
Job time: 3251 sec

Thu · Sep 5 10:01:18 2002

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